BIOVIEW California Wildlife Habitat Relationships - Version 8.1 File Species Info Single Condition Two Condition Element Info Habitat Info BioView Window Help Configure Habitat Data File Create/Edit Habitat Data File About Bioview

Bioview uses habitat suitability ratings from the CWHR database for user-selected species and applies them to a user-provided habitat data file. The habitat data file is generally a list of polygons in a Geographic Information System (GIS) data set representing habitats and stages for a forest or region or project area. However, the habitat data file need not necessarily represent a GIS layer. Bioview only requires a unique identifier for each habitat and stage for which a user wants a habitat suitability value for a given species. One advantage of Bioview over CWHR is that the user can provide habitat and stage selections in an input file rather than selecting them one-by-one as in a conventional CWHR query.

Bioview produces two types of output, each in two different formats. One output contains **Standard Habitat Suitability Values** for a given species from CWHR, except that they appear as integers rather than decimals – 0 or 1 for no suitability, 33 for low suitability, 66 for medium suitability and 100 for high suitability. Values are provided for reproduction, cover, feeding, the arithmetic mean of these three numbers and the geometric mean of these three numbers. The second output contains **Habitat Suitability Values Using Fuzzy Logic**. Each of these output types is available as a series of five comma-delimited text files (*.val files) or a single database file (*.dbf) with five fields.

Note that in Bioview, unlike in CWHR, the value for no suitability may be a 0 or a 1. A value of 1 is assigned when a habitat and stage has value for one or two of the life requisites, but not for all three. This convention was adopted to distinguish a habitat that provides some habitat value to a species, from one that doesn't have any. When a location has no value for any of the three life requisites, then a value of 0 is assigned. If you were to produce a Bioview GIS display of information for a species that has medium value for cover (value of 66), low value for forage (numeric value of 33), and no value for reproduction, the display for reproduction would show that the location had value for one or more of the other life requisites because of the presence of "1"s in the display

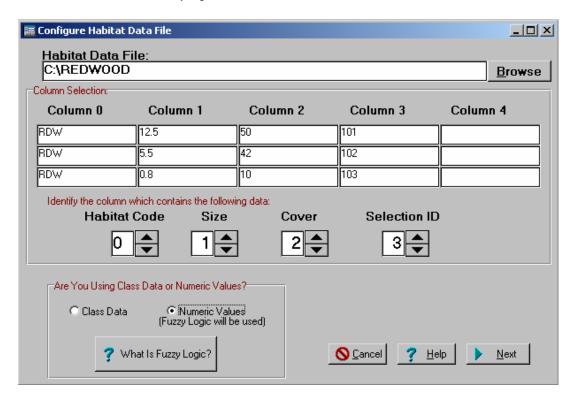
The two choices for Bioview on the main menu will both lead you through Bioview. Select "Configure Habitat Data File" if you already have a habitat data file in comma-delimited text format. Select "Create/Edit Habitat Data File" to create such a file. (For more information on preparing your data for use with Bioview and using Bioview output in a GIS, see Appendix A.)

Configure Habitat Data File

This window allows you to configure an existing habitat data file. First, click the **Browse** button to search for and select the habitat data file you wish to use. When you have done so, the selected file and its pathway will appear in the window at the top of the form. If the file is in the proper format, the columns below this window will fill in with data.

Next, use the spin boxes below these columns to identify which column contains each piece of required data. In the example, habitat code is found in Column 0, size in column 1, cover in column 2 and selection ID in column 3.

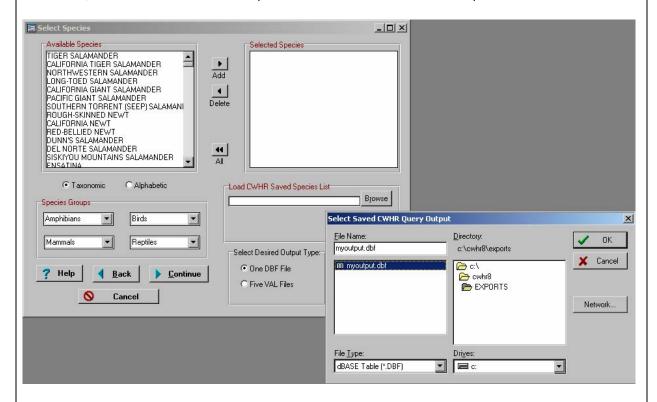
Finally, select the type of data that is contained in the file – class data or numeric values. Right-click using the mouse when a vertical arrow appears over either of these terms to see examples of class data or numeric values data. This is an important selection because fuzzy logic calculations can only be performed correctly on actual numeric values representing size and cover. For a description of what fuzzy logic is and how it is applied here, click on the button "What is fuzzy logic?"



The habitat data file above contains numeric values. The output files from this query will contain *Habitat Suitability Values Using Fuzzy Logic*.

Select Species

The species selection window appears next. Species are selected in a similar way as in CWHR queries except that here, by default, no species are selected. Use the radial buttons to sort the list taxonomically or alphabetically. To select a species, double-click on its name or highlight it and click the **Add** button. To remove species from the selected list, use the **Delete** button for one species at a time or the **All** button for all species at once.



Several species groups (i.e., passerines, bats, etc.) are available under the **Species Groups** drop boxes. Picking a group from the drop boxes will add the species in that category to the selected list.

You may also load a saved species list from a CWHR query and edit it using the **Delete** and **All** buttons. Doing this takes advantage of the query parameters in CWHR. For example, if you run CWHR first and save the output list to use later in Bioview, you will have had a chance to screen out those species which would not be present in your project area by virtue of their range in the state. Use the **Browse** button to search for and load a saved species list from a CWHR query. When you have done so, the selected file and its pathway will appear in the window next to the **Browse** button and the **Okay** button will be highlighted.

Finally, select the desired output type using the radial buttons in the lower right-hand corner of the form. Bioview will create either one database (*.dbf) file or five val (comma-delimited ascii text format) files for each species selected. The five val files include one output file each for reproduction, cover and feeding habitat suitability values, an output file for the <u>arithmetic mean</u> of these numbers and an output file for the <u>geometric mean</u> of these numbers. These files will automatically be saved into the same directory from which you loaded your habitat data file. One or five files, depending on your selection, will be named for each species using the following naming convention:

A048cvr.val - Cover Values

A048cvrf.val - Cover Values Using Fuzzy Logic

A048frg.val - Foraging or Feeding Values

A048frgf.val - Foraging or Feeding Values Using Fuzzy Logic

A048rpo.val - Reproduction Values

A048rpof.val – Reproduction Values Using Fuzzy Logic

A048arm.val – Arithmetic Mean

A048armf.val – Arithmetic Mean (Fuzzy)

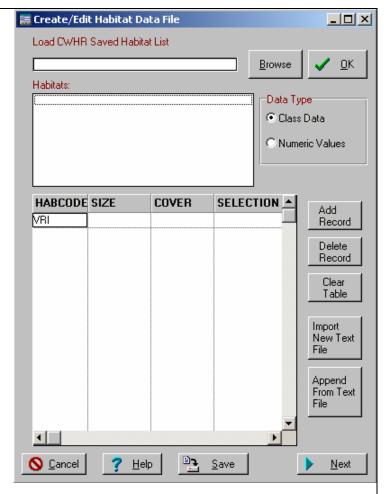
A048gdm val – Quadratic or Geometric Mean

Create/Edit Habitat Data File

Under this option, all the information for the habitat data file can be entered into a table and saved. Use the **Browse** then the **OK** button to search for and load a CWHR saved habitat list. This is not required but is provided as a convenient way to enter habitat codes into the new data file from a saved CWHR query. (A complete list of habitats, named "allhabs.dbf", has also been loaded into the default folder for retrieving.) If you select **Add Record** next to the table and then double click on one of the habitat names in the window above, its code will be placed in the table on the selected line.

Use the buttons to the right of the table to create and edit the file. Clear Table removes all data from the table. Add Record allows you to add to the table. Delete Record removes the currently selected record from the table. Import New Text File brings up a file selection window. Note that all information in the table will be removed if an import is performed. To simply append a file of existing records without deleting removing the table, use the Append From Text File button.

You may save your table at any time by using the **Save** button.



Before clicking **Next** to move to the species selection window, be sure the correct **Data Type** is selected near the top of the form. Data types and species selection are described above.

APPENDIX A: USING YOUR DATA WITH BIOVIEW

Configuring Your Data for Bioview

Bioview can only accept data in a comma-delimited ascii text format. This is a common export format from database and spreadsheet software programs. Be certain the program you export from does not install quotation marks ("") around data or extra spaces between commas. Microsoft Excel works well for both importing data in a variety of formats and exporting it as comma-delimited ascii text. It will give the exported file an extension of *.csv (stands for "comma-separated values"), which Bioview will easily read.

Export only the four columns of data needed by Bioview.

Note that, although Bioview allows you to point to the columns containing the data it requires, it runs best when the data is in the default configuration suggested by the **Configure Habitat Data File** window in the program:

The first column (Column 0) is the three-character code representing the habitat. (RIC is an exception. See table below.)

The second column (Column 1) is the size class. **Note that Bioview needs a value in this field, even for habitats that have no stages such as URB and BAR**. Insert a "1" where this is the case, even when using the numeric values/fuzzy logic option.

The third column (Column 2) is the cover class. If you are using a configuration other than the default, be certain this is not the final column of data. There are several habitats for which no cover classes are defined, such as URB and BAR. Also, size class 6, defined for many tree-dominated habitats such as SMC, does not have any corresponding cover classes. If these fields are empty for records or polygons representing such habitats, the final column of data in a comma-delimited ascii text file will be represented by a dangling comma. Bioview will search frantically for data that follows that comma and it will not find anything. The program will return an error message and you will not be able to continue. Also, for habitats that have no cover classes, be certain the cover class column does indeed have no data, rather than a "0", or the output will be incorrect. Bioview looks for data matches for both size and cover class values for species in a habitat and it returns values of "0" suitability for size and cover class combinations that do not exist in CWHR. For example, RDW 1D will show "0" suitability, even for a species you know finds suitability in RDW 1. You may have a numeric value in this field if you are using the numeric values/fuzzy logic option.

The fourth column (Column 3) is the selection ID, often the polygon ID in a GIS coverage.

Ideally, your data should look like this:

RDW,3,M,101

RDW,1,,102

Or, if you are using fuzzy logic, like this:

RDW,12.5,50,101

RDW, 0.8, 10, 102

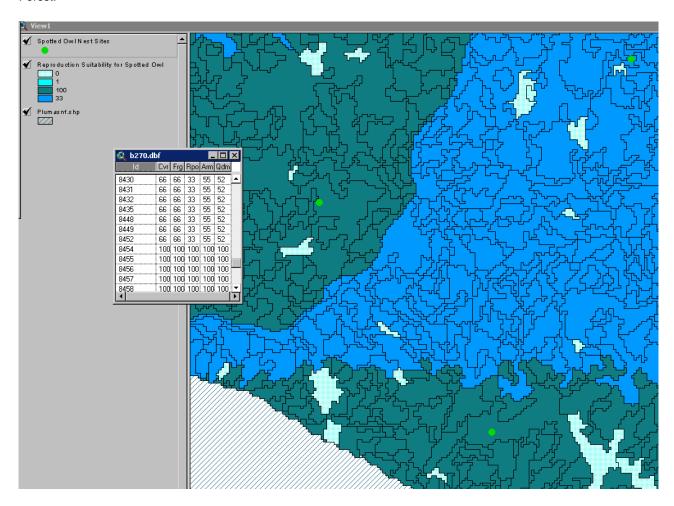
Using Numeric Values with the Fuzzy Logic Option

Below is a guide to the numeric values which should appear in the size and cover fields if you are using the fuzzy logic option.

Habitats	Size Column	Cover Column
Tree Habitats	dbh or QMD	% cover
Tree Habitats with No Cover Class (DOR,EOR)	dbh or QMD	
Herb Habitats	height	% cover
Aquatic Habitats	% time exposed	
Habitats with One Class (BAR, URB,DGR,IGR,IRH,IRF,VIN)	any value between 0 and 100	
Rice (RIC)		
This is a special case as cover values are defined for non-flooded rice habitat and depth values for flooded rice habitat. We have adopted the following new codes for RIC for Bioview only; the codes remain the same for all other CWHR queries.		
Rice, Non-flooded RIC 1A, 1B = RIN 1,2	% cover	
Rice, Flooded RIC 2S, 2M, 2D = RIF 1,2,3	depth	

Displaying Output Data from Bioview in a GIS

Displaying the results of your query spatially is beyond the programming language of CWHR Version 8.1 or Bioview. However, Bioview output is designed so that, for each species of interest, all habitat suitability values will appear in a single *.dbf table. Because the table contains the unique identifier for each polygon in your habitat data file, it can then be used to "attribute" the actual spatial data in a GIS. This is a simple process if you are familiar with popular GIS software programs such as ArcInfo or ArcView. A variety of habitat suitability maps can then be created for each species showing the range of values across a forest or region or project area, be it for reproduction, cover, feeding or an average of all three. Below, the Bioview output table b270.dbf is used to attribute a polygon coverage of habitats in an ArcView session to create a reproduction suitability map for the Spotted Owl in a section of Plumas National Forest.



APPENDIX B: FUZZY LOGIC AND ITS APPLICATION TO CWHR

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Some Background - Fuzzy Logic or Fuzzy Thinking?

Fuzzy Logic is a semi-popular term referring to an emerging branch of mathematics that is sometimes called multivalued set theory. This section is an attempt to describe the concepts and applications of this mathematics of uncertainty as it applies to wildlife habitat evaluations. The theoretical and mathematical underpinnings for fuzzy logic are clearly beyond the scope of this document. Although, for those with a serious interest in mathematical theory, the treatise "Fuzzy Sets and Fuzzy Logic: Theory and Applications" by George J. Klir and Bo Yuan (published by Prentice-Hall Inc. of New Jersey) is highly recommended.

In the simplest terms, fuzzy sets represent the mathematics of uncertainty, an emerging response to the recognition that little in the real, physical, and especially in the biological world is clear-cut and unambiguous. That the real world is only defined with uncertain, ambiguous, and incomplete data should be no surprise to those who regularly attempt to understand, explain, and/or manage natural systems. However, in many ways, such a reality is a recent discovery in the field of mathematics. From this recognition, and the "first" formalizations of a mathematics of uncertainty (fuzzy mathematics) by Lotfi Zadeh in the 1960's, has grown a respectable body of theory, proofs, and practice.

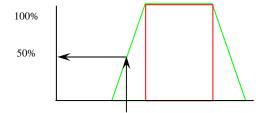
Fuzzy logic is not confused thinking, but a recognition that little in the world is clearly one thing or another. Fuzziness (not error) arises from classes of objects the boundaries of which cannot be well defined. A can of paint that contains no color but green is a member of the fuzzy class "green paint". As the proportion of green is reduced by the addition of blue dyes, the paint slowly begins to turn color. When is it not green? When is it "sea foam green" or cyan or turquoise? It could be conceived that when there is only green dye, membership in the class green paint is 100% and membership in the class blue paint is 0%. As blue dyes are added, the "blueness" of the paint increases (membership in class blue increases above 0) and at some point membership in the class green decreases. Turquoise, for example, could be described as a 65% member of the class blue and a 35% member of the class green.

Why Apply Fuzzy Logic to CWHR?

Fuzzy logic is ideally suited for application to the biological world where the differences (boundaries) between "things" are, at best, unclear. When is an erect woody plant a tree rather than a bush? When is a forest great habitat, versus good habitat or poor habitat? The kind of habitat represented by a forest with an average stand diameter of 45 inches and a crown cover of 90% is very different from a dense thicket of young trees whose average diameter is 4 inches, and crown cover 90%. But, does a forest with an average stand diameter of 12 inches represent a different quality of habitat than one with a diameter of 10 inches? Probably not, at least in the real world. This question identifies the fuzzy nature of the CWHR habitat suitability models.

The CWHR models use environmental variables expressed as classes (crown decadence and percent ground cover for shrub habitats), with a suitability rating for each combination. These classes are fuzzy sets with unclear and ambiguous boundaries. Bioview applies fuzzy logic to these classes to provide a more realistic evaluation of habitat suitability.

The figure to the right represents a single CWHR class (of any variable) with the vertical lines the CWHR class boundaries. Maximum membership is 100% and all values of the variable on the x-axis between the vertical lines are 100% members in the class. Values that fall between the vertical and the slanting lines are partial members of the class. Their degree of membership is determined by where their vertical extension intersects the diagonal line. In this example degree of membership in this specific class is just less than 50%. Values outside the slanted lines have zero membership in the class. Any value can have

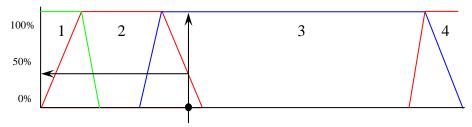


partial or complete membership in one or more additional classes as explained below.

How is Fuzzy Logic Applied to CWHR in Bioview?

Bioview applies a linear boundary for the fuzziness although any shape, including logarithmic and sigmoid, is appropriate as long as it represents the change in uncertainty with closeness to the boundary. For many sets the fuzziness can be calculated or measured and the best shape derived.

By extending the previous diagram to cover the full range of a variable (e.g., size class for forests) it becomes obvious that every point is a member in at least one class. Points that fall in the fuzzy regions, defined by the



slanted lines, are members in two classes. The point illustrated is a full member of Size Class 3 and about a 40% member of Size Class 2. If, in this example, the habitat value for Northern Goshawk is high in Class 3 and medium in class 2 the actual value of the habitat lies somewhere between medium and high. Size Class 3 contributes a full membership in a set of high habitat value and Size Class 2 contributes a 35% membership in a medium value. The net value (from size alone) is a balance of the two.

However, CWHR does not use just one variable for determining habitat suitability. In the case of forests there are two, size and cover. And there is a CWHR model for every combination of those two variables. Because fuzzy sets can be combined in any number, Bioview evaluates the variation in habitat suitability with size and cover independently, and then combines them in one "unfuzzied" value.